IN THE SEQUENCE LISTING:

Please amend the sequence listing to add SEQ ID NOS; 35-38 as follows:

<210> 35
<211> 1749
<212> DNA
<213> Arabidopsis thaliana

<400> 35
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TACCTACTCA AAGAATGCTA TAAACATGGT AGCTTGAAGG CAACAAAAAA GTTCCAAGCT 180
TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAGGACC TGCTACTTTC 240
ATTATTAATT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT 300
TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA 360
GATATTTGTT TGGCGAGAAA GCTAGCTGCT CAGTTCTTCC TTGCTACTGT TGGTGGATCT 420
TTAACTTATG ATGAGAAGGT TATGGTGCAT ACTCTTAGAG TGTTTGATGT GAGGTTAACT 480
AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGGA 540
AATGCGTTTC TGGAACAATA CATTTCTGAC TTGATCAAGT CGAAATCTTT CATGACGGCT 600
GTGACTCTGT TAGAGCATTT CTCTTTCCGT TTCCCTGGAG AAACTTTTCT TCAACAAATG 660
GTTGAGGATA AAAATTTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGGCCAAGT 720
TTATGCATTC TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAATATC 780
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GCTCTGAAGG TTCTAGCAGA AAAAGCATGT TGGGATGTTG CTGAAATTAA GACAAAAGGT 900
GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGCAGTGG AAGCTGGATA CTTGGAGAAG 960
GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020
GTTGCTTTTG TTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGTAGA AGATGTAGTT 1080
TGGGTTGATG AAGTCAACGA GTTGAGAAAA GCAACTTCTT TTCTTGAAGG ATGTAGAGTT 1140
GTGGGTATTG ACTGTGAATG GAAACCTAAT TATATTAAAG GCAGTAAACA GAACAAGGTT 1200
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TTAAAGCTCG TCTCTCTGAC TGAGGATTAC CCTGATCATA AATTATCCTC AGGTTACAAT 1380
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TACGACATGT TGCTAGACAT TCAAAATGTT TTTAATGAAC CATTTGGTGG TTTAGCAGGA 1500
CTAACGAAGA AAATATTGGG AGTGTCTTTG AACAAAACAA GACGCAATAG CGACTGGGAA 1560
CAAAGGCCTT TGAGCCAGAA TCAGCTTGAG TATGCTGCTC TTGATGCTGC AGTGTTGATT 1620
CACATATTTC GCCATGTTCG CGATCATCCT CCACATGACA GTAGTTCAGA GACAACCCAG 1680
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<211> 582
<212> PRT
<213> Arabidopsis thaliana

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Tyr Val Ser Pro Val Val Phe Leu Tyr Leu Leu Lys Glu Cys Tyr Lys
35 40 45

His Gly Ser Leu Lys Ala Thr Lys Lys Phe Gln Ala Leu Gln Tyr Gln
50 55 60

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Val His Arg Val Leu Ala Asn Lys Pro Gln Pro Gly Pro Ala Thr Phe
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Ile Ile Asn Cys Leu Thr Leu Leu Pro Leu Phe Gly Val Tyr Gly Glu
                85                  90                  95

Gly Phe Ser His Leu Val Ile Ser Ala Leu Arg Arg Phe Phe Lys Thr
            100                 105                 110

Val Ser Glu Pro Thr Ser Glu Glu Asp Ile Cys Leu Ala Arg Lys Leu
        115                 120                 125

Ala Ala Gln Phe Phe Leu Ala Thr Val Gly Gly Ser Leu Thr Tyr Asp
    130                 135                 140

Glu Lys Val Met Val His Thr Leu Arg Val Phe Asp Val Arg Leu Thr
145                 150                 155                 160

Ser Ile Asp Glu Ala Leu Ser Ile Ser Glu Val Trp Gln Arg Tyr Gly
                165                 170                 175

Phe Ala Cys Gly Asn Ala Phe Leu Glu Gln Tyr Ile Ser Asp Leu Ile
            180                 185                 190

Lys Ser Lys Ser Phe Met Thr Ala Val Thr Leu Leu Glu His Phe Ser
        195                 200                 205

Phe Arg Phe Pro Gly Glu Thr Phe Leu Gln Gln Met Val Glu Asp Lys
    210                 215                 220

Asn Phe Gln Ala Ala Glu Arg Trp Ala Thr Phe Met Gly Arg Pro Ser
225                 230                 235                 240

Leu Cys Ile Leu Val Gln Glu Tyr Gly Ser Arg Asn Met Leu Lys Gln
                245                 250                 255

Ala Tyr Asn Ile Ile Asn Lys Asn Tyr Leu Gln His Asp Phe Pro Glu
            260                 265                 270

Leu Tyr His Lys Cys Lys Glu Ser Ala Leu Lys Val Leu Ala Glu Lys
        275                 280                 285

Ala Cys Trp Asp Val Ala Glu Ile Lys Thr Lys Gly Asp Arg Gln Leu
    290                 295                 300

Leu Lys Tyr Leu Val Tyr Leu Ala Val Glu Ala Gly Tyr Leu Glu Lys
305                 310                 315                 320

Val Asp Glu Leu Cys Asp Arg Tyr Ser Leu Gln Gly Leu Pro Lys Ala
                325                 330                 335

Arg Glu Ala Glu Val Ala Phe Val Glu Lys Ser Phe Leu Arg Leu Asn
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Asp Leu Ala Val Glu Asp Val Val Trp Val Asp Glu Val Asn Glu Leu
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Arg Lys Ala Thr Ser Phe Leu Glu Gly Cys Arg Val Val Gly Ile Asp
    370                 375                 380

Cys Glu Trp Lys Pro Asn Tyr Ile Lys Gly Ser Lys Gln Asn Lys Val
385                 390                 395                 400

Ser Ile Met Gln Ile Gly Ser Asp Thr Lys Ile Phe Ile Leu Asp Leu
                405                 410                 415

Ile Lys Leu Tyr Asn Asp Ala Ser Glu Ile Leu Asp Asn Cys Leu Ser
            420                 425                 430

His Ile Leu Gln Ser Lys Ser Thr Leu Lys Leu Val Ser Leu Thr Glu
        435                 440                 445

Asp Tyr Pro Asp His Lys Leu Ser Ser Gly Tyr Asn Phe Gln Cys Asp
    450                 455                 460

Ile Lys Gln Leu Ala Leu Ser Tyr Gly Asp Leu Lys Cys Phe Glu Arg
465                 470                 475                 480

Tyr Asp Met Leu Leu Asp Ile Gln Asn Val Phe Asn Glu Pro Phe Gly
                485                 490                 495

Gly Leu Ala Gly Leu Thr Lys Lys Ile Leu Gly Val Ser Leu Asn Lys
            500                 505                 510

Thr Arg Arg Asn Ser Asp Trp Glu Gln Arg Pro Leu Ser Gln Asn Gln
        515                 520                 525

Leu Glu Tyr Ala Ala Leu Asp Ala Ala Val Leu Ile His Ile Phe Arg
    530                 535                 540

His Val Arg Asp His Pro Pro His Asp Ser Ser Ser Glu Thr Thr Gln
545                 550                 555                 560

Trp Lys Ser His Ile Val Ser Thr Ser Tyr Lys Ser Pro Tyr Leu Ser
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Ser Asp Asn Ser Arg Arg
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<210> 37
<211> 1518
<212> DNA
<213> Arabidopsis thaliana

<400> 37

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CACTCCAATA CGTCGTCGTT TCCGACCGTC ACTCTCCTCC AAGTCGCATG CCGACTCAGT     180
CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTTGA GTTCGATTCA TCTTCCATCG     240
GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG     300
TTTAAACAGG ATTTGGTTTA CTTGTCTTCG ACATTTACTC AACATGGATG TGAAGGTGGA     360
TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG     420
CGGTTTGGGA GAAAGGCGCC AAAGGATATC AAGAGCTTGG CTGCTATATG TAAGGAAATG     480
CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCATATCG TCCTCTTACA     540
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AAGGCTACAG ATGTAATCAG ATCAATGTCG GAAAATGGTC AAAACATAGC CAATGGAGTG     780
GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC     840
AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG     900
AAGAAAACAA GAAGACGTGT CGCCTCAAGC ACTATGAACA CAAATAAGCA GTTGGTCTGT     960
TCTGCGGACT GGCAAGGTCC ACCGCCATGG GACTCATCTT TAGGCGGTGA TGGCTGCCCT    1020
AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TGTGGGGATT    1080
GATGCTGCAA TCCCACACTC AAAGAAGCCG GATTCAAGGG AGTTGCTTGA TCAAGCATTC    1140
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AAGCATCAAA TATATCGAGT AAAGAGTCTT CTTAAAAATG AGCAGCTACT TGAGGTGATA    1260
GAGACTTTCC AGCTAAAGAT CAGCGGAAAT CAGCTGATGT CCAGATGTAC GAAGTGCAAT    1320
GGGAAATTTA TTCAGAAACC TCTAAGCATT GAAGAAGCTA TTGAAGCAGC AAAGGGTTTC    1380
CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAGTG CATGAACTGC    1440
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<212> PRT
<213> Arabidopsis thaliana

<400> 38

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Leu Asp Ala Glu Trp Lys Pro Gln His Ser Asn Thr Ser Ser Phe Pro
        35                  40                  45

Thr Val Thr Leu Leu Gln Val Ala Cys Arg Leu Ser His Ala Thr Asp
    50                  55                  60

Val Ser Asp Val Phe Leu Ile Asp Leu Ser Ser Ile His Leu Pro Ser
65                  70                  75                  80

Val Trp Glu Leu Leu Asn Asp Met Phe Val Ser Pro Asp Val Leu Lys
                85                  90                  95

Leu Gly Phe Arg Phe Lys Gln Asp Leu Val Tyr Leu Ser Ser Thr Phe
            100                 105                 110

Thr Gln His Gly Cys Glu Gly Gly Phe Gln Glu Val Lys Gln Tyr Leu
        115                 120                 125

Asp Ile Thr Ser Ile Tyr Asn Tyr Leu Gln His Lys Arg Phe Gly Arg
    130                 135                 140

Lys Ala Pro Lys Asp Ile Lys Ser Leu Ala Ala Ile Cys Lys Glu Met
145                 150                 155                 160

Leu Asp Ile Ser Leu Ser Lys Glu Leu Gln Cys Ser Asp Trp Ser Tyr
                165                 170                 175

Arg Pro Leu Thr Glu Glu Gln Lys Leu Tyr Ala Ala Thr Asp Ala His
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            180                 185                 190

Cys Leu Leu Gln Ile Phe Asp Val Phe Glu Ala His Leu Val Glu Gly
        195                 200                 205

Ile Thr Val Gln Asp Leu Arg Val Ile Asn Val Gly Leu Gln Glu Ile
    210                 215                 220

Leu Thr Glu Ser Asp Tyr Ser Ser Lys Ile Val Thr Val Lys Leu Cys
225                 230                 235                 240

Lys Ala Thr Asp Val Ile Arg Ser Met Ser Glu Asn Gly Gln Asn Ile
                245                 250                 255

Ala Asn Gly Val Val Pro Arg Lys Thr Thr Leu Asn Thr Met Pro Met
            260                 265                 270

Asp Glu Asn Leu Leu Lys Ile Val Arg Lys Phe Gly Glu Arg Ile Leu
        275                 280                 285

Leu Lys Glu Ser Asp Leu Leu Pro Lys Lys Leu Lys Lys Lys Thr Arg
    290                 295                 300

Arg Arg Val Ala Ser Ser Thr Met Asn Thr Asn Lys Gln Leu Val Cys
305                 310                 315                 320

Ser Ala Asp Trp Gln Gly Pro Pro Pro Trp Asp Ser Ser Leu Gly Gly
                325                 330                 335

Asp Gly Cys Pro Lys Phe Leu Leu Asp Val Met Val Glu Gly Leu Ala
            340                 345                 350

Lys His Leu Arg Cys Val Gly Ile Asp Ala Ala Ile Pro His Ser Lys
        355                 360                 365

Lys Pro Asp Ser Arg Glu Leu Leu Asp Gln Ala Phe Lys Glu Asn Arg
    370                 375                 380

Val Leu Leu Thr Arg Asp Thr Lys Leu Leu Arg His Gln Asp Leu Ala
385                 390                 395                 400

Lys His Gln Ile Tyr Arg Val Lys Ser Leu Leu Lys Asn Glu Gln Leu
                405                 410                 415

Leu Glu Val Ile Glu Thr Phe Gln Leu Lys Ile Ser Gly Asn Gln Leu
            420                 425                 430

Met Ser Arg Cys Thr Lys Cys Asn Gly Lys Phe Ile Gln Lys Pro Leu
        435                 440                 445

Ser Ile Glu Glu Ala Ile Glu Ala Ala Lys Gly Phe Gln Arg Ile Pro
    450                 455                 460

Asn Cys Leu Phe Asn Lys Asn Leu Glu Phe Trp Gln Cys Met Asn Cys
465                 470                 475                 480

His Gln Leu Tyr Trp Glu Gly Thr Gln Tyr His Asn Ala Val Gln Lys
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485 490 495

Phe Met Glu Val Cys Lys Leu Ser Glu
500 505